

AMENDMENTS TO THE CLAIMS

1. (Withdrawn) An isolated polypeptide having an enzymatic glycosyltransferase activity capable of forming dextrans having $\alpha(1 \rightarrow 2)$ linkages from saccharose, α -D-fluoroglucose, paranitrophenyl- α -D glucopyranoside, α -D-glucopyranoside- α -D sorbofuranoside or 4-O- α -D galactopyranosylsucrose, characterized in that it comprises at least one glucan binding domain and a catalytic activity domain located downstream of the glucan binding domain.

2. (Withdrawn) A polypeptide according to claim 1, comprising at least two catalytic domains located either side of the glucan binding domain.

3. (Withdrawn) A polypeptide according to claim 1 or claim 2, comprising a peptide signal, a variable zone, two catalytic domains and a glucan binding domain located between the two catalytic domains.

4. (Withdrawn) A polypeptide according to one of claims 1 to 3, in which the domain or domains with a catalytic activity has/have a percentage similarity in the range of 65% to 100% with SEQ ID NO:1.

5. (Withdrawn) A polypeptide according to one of the preceding claims, in which the size of the glucan binding domain is more than 500 amino acids.

6. (Withdrawn) A polypeptide according to claim 5, containing SEQ ID No:2.

7. (Withdrawn) A polypeptide according to claim 6, modified by substitution, insertion or deletion of amino acid sequences and comprising sequences having at least 80% and preferably at least 90% similarity with the following sequences of SEQ ID No.2:

423-439 (SEQ ID No:6)	2120-2138 (SEQ ID No:12)
478-501 (SEQ ID No:7)	2161-2184 (SEQ ID No:13)
519-539 (SEQ ID No:8)	2202-2214 (SEQ ID No:14)
560-571 (SEQ ID No:9)	2243-2250 (SEQ ID No:15)
631-645 (SEQ ID No:10)	2315-2322(SEQ ID No:16)
1014-1021 (SEQ ID No:11)	2689-2696(SEQ ID No:17).

8. (Withdrawn) A polypeptide according to claim 7, in which the following amino acids are unchanged:

W in positions 425 and 2122;
E in positions 430, 565 and 2127,2248;
D in positions 487, 489, 527, 638, 2170, 2172, 2210 and 2322;
H in position 637 and 2321;
Q in position 1019 and 2694.

9. (Currently Amended) An isolated nucleic acid encoding an enzyme with glycosyltransferase activity that can form dextrans having $\alpha(1\rightarrow2)$ linkages from saccharose, α -D-fluoroglucose, paranitrophenyl- α -D glucopyranoside, α -D-glucopyranoside- α -D sorbofuranoside or 4-O- α -D galactopyranosylsucrose and comprising at least one nucleotide sequence encoding a catalytic domain having at least 50%, preferably at least 80% identity with SEQ ID No:3 and located 3' of a sequence encoding a glucan binding domain.

10. (Currently Amended) A The isolated nucleic acid according to claim 9, comprising:
- two sequences encoding catalytic domains having ~~at least 50%, preferably at~~ least 80% identity with SEQ ID No: 3;
 - a sequence encoding the glucan binding domain, ~~the latter preferably being located between the two sequences in a).~~
11. (Currently Amended) ~~An~~ The isolated nucleic acid according to claim 10, having at least 80% identity with:
- SEQ ID No:4; or
 - ~~the~~ a complementary strand to SEQ ID No: 4 ~~the sequence in a);~~ or
 - a sequence hybridizing to SEQ ID No: 4 or a complementary strand to SEQ ID No: 4 ~~a) or b)~~ under stringent conditions.
12. (Currently Amended) ~~An isolated nucleic acid according to claim 11, constituted by comprising~~ SEQ ID No:4 or its complementary strand ~~or the sequence deduced from degeneracy of the genetic code.~~
13. (Currently Amended) ~~An~~ The isolated nucleic acid according to claim 11 comprising:
- a sequence having at least 80% identity with the sequence encoding a dextransucrase expressed by the plasmid pCR-Ty-dsrD deposited at the CNCM on 15th March 2001 with accession number I-2649; or
 - a complementary sequence to the sequence in a).
14. (Previously Presented) An expression vector comprising a nucleic acid according to any one of claims 9 to 13.

15. (Currently Amended) A The expression vector according to claim 14, in which the nucleic acid is under the control of a sequence allowing its expression in prokaryotic or eukaryotic cells.

16. (Previously Presented) A host cell transformed by a nucleic acid according to ~~one of~~ ~~claims 9 to 13~~ claim 9 or a vector according to claim 14 ~~or claim 15~~.

17. (Currently Amended) A The transformed host cell according to claim 16, selected from the group comprising E. coli, Leuconostocci, plants, Lactococci and Bacilli or yeasts.

18. (Currently Amended) A The transformed host cell according to claim 17, ~~characterized in that it~~ wherein said transformed host cell is a strain of E. coli deposited at the CNCM on 15th March 2001 with accession number I-2649.

19. (Withdrawn) A method for producing a dextransucrase that can form $\alpha(1 \rightarrow 2)$ bonds, comprising:

- a) inserting a nucleic acids according to one of claims 9 to 13 or a vector according to claim 14 or claim 15 into a host cell according to claim 16;
- b) purifying the enzyme from a cell extract.

20. (Withdrawn) A method according to claim 19, in which the host cell is a prokaryote selected from a group comprising E. coli, Lactococci, Bacilli and Leuconostocci.

21. (Withdrawn) A method according to claim 19, in which the host cell is a eukaryote selected from a group comprising yeasts, fungi and plants.

22. (Withdrawn) A method for obtaining a dextransucrase that can form oligosides or dextrans having a percentage of $\alpha(1\rightarrow2)$ bonds of more than 30% of the total bonds, comprising a step for modifying SEQ ID No:4 by addition, deletion or mutation provided that:

- the reading frame is not modified; and
- the following amino acids are conserved after translation:
 - W in positions 425 or 2122, encoded by the TGG triplet in positions 1273 and 6364;
 - E in positions 430, 565, 2127 and 2248, encoded by GAA triplets in positions 1288, 1693, 6379 and 6742 respectively;
 - D in positions 487, 489, 527, 638, 2170 and 2210, encoded by GAT triplets in positions 1459, 1465, 1579, 1912, 6508 and 6628 respectively;
 - D in positions 2172 and 2322 encoded by GAT triplets in positions 6514 and 6964;
 - H in position 637 and 2321, respectively encoded by the CAT triplet in position 1909 and CAC in position 6961;
 - Q in positions 1019 and 2694, respectively encoded by triplets CAA (position 3055) and CAG (position 8080).

23. (Withdrawn) A method for obtaining an isolated glycosyltransferase that can form oligosides or dextrans having more than 30% of $\alpha(1\rightarrow2)$ bonds, comprising:

- a step for randomly modifying SEQ ID No: 4 and establishing a library of variations;
- a step for expressing a host housing a variation from said modified sequences in a suitable host cell;
- a step for screening hosts expressing an enzyme that can form more 30% of $\alpha(1\rightarrow2)$ bonds on a suitable substrate;
- a step for isolating the improved gene or genes.

24. (Withdrawn) A glycosyltransferase that can form at least 30% of $\alpha(1\rightarrow2)$ bonds that can be obtained by a method according to one of claims 19 to 22.

25. (Withdrawn) Use of a glycosyltransferase obtained by a method according to one of claims 19 to 22 in the production of a composition with a prebiotic effect.

26. (Withdrawn) Use of a glycosyltransferase obtained by a method according to one of claims 19 to 23 in the production of a pharmaceutical or cosmetic composition.
domain is between said two sequences encoding said catalytic domains.

28. (New) An isolated nucleic acid encoding an enzyme with glycosyltransferase activity that can form dextrans having $\alpha(1\rightarrow2)$ linkages from saccharose, α -D-fluoroglucose, paranitrophenyl- α -D glucopyranoside, α -D-glucopyranoside- α -D sorbofuranoside or 4-O- α -D galactopyranosylsucrose and comprising at least one nucleotide sequence encoding a catalytic domain of SEQ ID No:3 and located 3' of a sequence encoding a glucan binding domain.

29. (New) An isolated nucleic acid consisting of SEQ ID No:4 or its complementary strand.

30. (New) A host cell transformed by a nucleic acid according to claim 10.

31. (New) A host cell transformed by a nucleic acid according to claim 11.

32. (New) A host cell transformed by a nucleic acid according to claim 12.

33. (New) A host cell transformed by a nucleic acid according to claim 13.

34. (New) A host cell transformed by a vector according to claim 14.

35. (New) A host cell transformed by a vector according to claim 15.